

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**LISTING OF CLAIMS:**

Claim 1 (Original): An isolated nucleic acid consisting of a nucleotide sequence set forth in SEQ ID NO: 2 or SEQ ID NO: 22.

Claim 2 (Original): A primer for the detection of cucumber mosaic virus (CMV)-resistant plants, which comprises consecutive nucleotides selected from a nucleotide sequence set forth in SEQ ID NO: 2 or SEQ ID NO: 22.

Claim 3 (Original): The primer of Claim 2, wherein the primer has a nucleotide sequence selected from SEQ ID NO: 1 and SEQ ID NO: 23 to SEQ ID NO: 28.

Claim 4 (Currently Amended): A kit for the detection of CMV-resistant plant, which comprises the nucleic acid of Claim 1 ~~or the primer of Claim 2~~.

Claim 5 (Currently Amended): A method for the detection of a CMV-resistant plant, comprising the step of analyzing the genomic DNA of a plant in the presence of the nucleic acid of Claim 1 ~~or the primer of Claim 2~~.

Claim 6 (Original): The method of Claim 5, wherein the analysis is performed by any one method selected from the group consisting of RFLP (restriction fragment length polymorphism), RAPD (randomly amplified polymorphic DNA), DAF (DNA amplification fingerprinting), AP-PCR (arbitrarily primed PCR), STS (sequence tagged site), EST (expressed sequence tag), SCAR (sequence characterized amplified regions), ISSR (inter-simple sequence repeat amplification), AFLP

(amplified fragment length polymorphism), CAPS (cleaved amplified polymorphic sequence) and PCR-SSCP (PCR-single strand conformation polymorphism).

Claim 7 (Original): The method of Claim 5, wherein the plant is selected from the group consisting of cucumber, watermelon, red pepper, melon, Chinese cabbage, tobacco, Petunia, cotton, and rose.

Claim 8 (Currently Amended): A method for determining the genotype of a CMV-resistant plant, comprising the step of analyzing the genomic DNA of a plant in the presence of the nucleic acid of Claim 1 ~~or the primer of Claim 2.~~

Claim 9 (Original): The method of Claim 8, wherein the analysis is performed by any one method selected from the group consisting of RFLP (restriction fragment length polymorphism), RAPD (randomly amplified polymorphic DNA), DAF (DNA amplification fingerprinting), AP-PCR (arbitrarily primed PCR), STS (sequence tagged site), EST (expressed sequence tag), SCAR (sequence characterized amplified regions), ISSR (inter-simple sequence repeat amplification), AFLP (amplified fragment length polymorphism), CAPS (cleaved amplified polymorphic sequence), and PCR-SSCP (PCR-single strand conformation polymorphism).

Claim 10 (Original): The method of Claim 8, wherein the plant is selected from the group consisting of cucumber, watermelon, red pepper, melon, Chinese cabbage, tobacco, Petunia, cotton, and rose.

Claim 11 (Original): A CMV-resistant plant which reproduces asexually by tissue culture and comprises a nucleic acid consisting of a nucleotide sequence set forth in SEQ ID NO: 2 or SEQ ID NO: 22.

Claim 12 (Original): The CMV-resistant plant of Claim 11, wherein the plant is selected from the group consisting of cucumber, watermelon, red pepper, melon, Chinese cabbage, tobacco, Petunia, cotton, and rose.

Claim 13 (Currently Amended): A seed which is obtained from the CMV-resistant plant of Claim 11 ~~or claim 12~~ and comprises a nucleic acid consisting of a nucleotide sequence set forth in SEQ ID NO: 2 or SEQ ID NO: 22.

Claim 14 (New): A kit for the detection of CMV-resistant plant, which comprises the primer of Claim 2.

Claim 15 (New): A method for the detection of a CMV-resistant plant, comprising the step of analyzing the genomic DNA of a plant in the presence of the primer of Claim 2.

Claim 16 (New): A method for determining the genotype of a CMV-resistant plant, comprising the step of analyzing the genomic DNA of a plant in the presence of the primer of Claim 2.

Claim 17 (New): A seed which is obtained from the CMV-resistant plant of Claim 12 and comprises a nucleic acid consisting of a nucleotide sequence set forth in SEQ ID NO: 2 or SEQ ID NO: 22.